

IN THE CLAIMS:

1-2. (canceled)

3. (original) A method of detecting human papillomavirus (HPV) genome, comprising performing a polymerase chain reaction for genomic DNA contained in a biological sample using one or more primer pairs selected from among pairs of primers capable of complementarily binding to the HPV genome and having nucleotide sequences represented by SEQ ID Nos. 1 and 2, SEQ ID Nos. 3 and 4, SEQ ID Nos. 5 and 6, and SEQ ID Nos. 7 and 8.

4. (original) The method as set forth in claim 3, wherein an HPV 11 L1 gene is detected using the primer pair having the nucleotide sequences represented by SEQ ID Nos. 1 and 2.

5. (original) The method as set forth in claim 3, wherein an HPV 16 L1 gene is detected using the primer pair having the nucleotide sequences represented by SEQ ID Nos. 3 and 4.

6. (original) The method as set forth in claim 3, wherein an HPV 18 L1 gene is detected using the primer pair having the nucleotide sequences represented by SEQ ID Nos. 5 and 6.

7. (original) The method as set forth in claim 3, wherein an HPV 31 L1 gene is detected using the primer pair having the nucleotide sequences represented by SEQ ID Nos. 7 and 8.

8. (canceled)